

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/813,290

DATE: 09/10/2001

TIME: 11:11:54

Input Set : A:\LEX-0151-USA SEQLIST.txt

Output Set: N:\CRF3\09102001\I813290.raw

ENTERED

4 <110> APPLICANT: Walke, D. Wade
 5 Wilganowski, Nathaniel L.
 6 Turner, C. Alexander Jr.
 7 Hilbun, Erin
 8 Wang, Xiaoming
 9 Donoho, Gregory
 10 Scoville, John
 12 <120> TITLE OF INVENTION: Novel Human Secreted Proteins and Polynucleotides Encoding
 the Same

14 <130> FILE REFERENCE: LEX-0151-USA
 C--> 16 <140> CURRENT APPLICATION NUMBER: US/09/813,290 ✓
 C--> 16 <141> CURRENT FILING DATE: 2001-03-20
 16 <150> PRIOR APPLICATION NUMBER: US 60/190,638
 17 <151> PRIOR FILING DATE: 2000-03-20
 19 <150> PRIOR APPLICATION NUMBER: US 60/191,188
 20 <151> PRIOR FILING DATE: 2000-03-22
 22 <150> PRIOR APPLICATION NUMBER: US 60/193,639
 23 <151> PRIOR FILING DATE: 2000-03-31
 25 <160> NUMBER OF SEQ ID NOS: 10
 27 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 2628
 31 <212> TYPE: DNA
 32 <213> ORGANISM: homo sapiens
 34 <400> SEQUENCE: 1

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 37 ctccttctct cctccgcccc tcttcccgcc caggactggg tggagccact gccttataag 180
 38 tgggtggcctg gtggcagcag agcaaactac aaccggcgcc cagcgggacc agaggcgccg 240
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 40 atttgctggc tgctaggggg cctcctgctc catgggggta gctctggccc cagccccggc 360
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 42 atctttctgg gccccaggg ctccctgaac ctccaggcca tgtacctaga tgagtaccga 480
 43 gaccgcctct ttctgggtgg cctggacgcc ctctactctc tgcggctgga ccaggcatgg 540
 44 ccagatcccc gggaggtcct gtggccaccg cagccaggac agaggaggga gtgtgttcga 600
 45 aagggaagag atcctttgac agagtgcgcc aacttcgtgc ggggtgctaca gcctcacaa 660
 46 cggacccacc tgctagcctg tggcactggg gccttcacag ccacctgtgc cctcatcaca 720
 47 gttggccacc gtggggagca tgtgctccac ctggagcctg gcagtgtgga aagtggccgg 780
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 49 tacacgggtc tctactgtga cttcctgggg cgagaggcca tgatcttccg aagtggaggt 900
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 51 atggccgccc ggatccctga gaactctgac caggacaatg acaaggtgta cttcttcttc 1020
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 57 gacatctggg aggttttcaa cgggcccttt gccaccgag atgggcctca gcaccagtgg 1380

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60 gcccagagccc acccctcat gttctggcct gtgcggcctc gacatggccg cctgtcctt 1560
61 gtcaagaccc acctggccca gcagctacac cagatcgtgg tggaccgcgt ggaggcagag 1620
62 gatgggacct acgatgtcat ttctctgggg actgactcag ggtctgtgct caaagtcac 1680
63 gctctccagg cagggggctc agctgaacct gaggaagtgg ttctggagga gctccagggtg 1740
64 ttttaaggtgc caacacctat caccgaaatg gagatctctg tcaaaaggca aatgctatac 1800
65 gtgggctctc ggctgggtgt ggcccagctg cggtgcacc aatgtgagac ttacggcact 1860
66 gcctgtgcag agtgcctcct ggcccgggac ccatactgtg cctgggatgg tgccctcctgt 1920
67 acccactacc gcccagcct tggcaagcgc cggttccgcc ggcaggacat ccggcacggc 1980
68 aaccctgccc tgcagtgcct gggccagagc caggaagaag aggcagtggg acttgtggca 2040
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70 ccccgctgct ctgtgcgtg gctcttgca agggcagggg atgagggggc tgaccagggtg 2160
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76 cgcgtgtggt gcaggggcac caaggaaatgc tcaggctgct tccggagccg gagccggggc 2520
77 aagcaggcca ggggcaagag ctgggcaggg ctggagctag gcaagaagat gaagagccgg 2580
78 gtgcatgccg agcacaatcg gacgccccgg gaggtggagg ccacgtag 2628

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80 <210> SEQ ID NO: 2

81 <211> LENGTH: 875

82 <212> TYPE: PRT

83 <213> ORGANISM: homo sapiens

85 <400> SEQUENCE: 2

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88 Val Trp His Lys Ser Leu His Trp Ala Asn Lys Val Glu Gly Glu Ala
89 20 25 30
90 Ala Gly Gly Arg Gln Gly Pro Ser Leu Leu Leu Ser Ser Ala Pro Leu
91 35 40 45
92 Pro Ala Gln Asp Trp Val Glu Pro Leu Pro Tyr Lys Trp Trp Pro Gly
93 50 55 60
94 Gly Ser Arg Ala Asn Tyr Asn Arg Arg Pro Ala Gly Pro Glu Gly Gly
95 65 70 75 80
96 Ser Ala Gly Arg Arg Gln Arg Cys Pro Gln Phe Pro Ser Met Ala Pro
97 85 90 95
98 Ser Ala Trp Ala Ile Cys Trp Leu Leu Gly Gly Leu Leu Leu His Gly
99 100 105 110
100 Gly Ser Ser Gly Pro Ser Pro Gly Pro Ser Val Pro Arg Leu Arg Leu
101 115 120 125
102 Ser Tyr Arg Asp Leu Leu Ser Ala Asn Arg Ser Ala Ile Phe Leu Gly
103 130 135 140
104 Pro Gln Gly Ser Leu Asn Leu Gln Ala Met Tyr Leu Asp Glu Tyr Arg
105 145 150 155 160
106 Asp Arg Leu Phe Leu Gly Gly Leu Asp Ala Leu Tyr Ser Leu Arg Leu
107 165 170 175
108 Asp Gln Ala Trp Pro Asp Pro Arg Glu Val Leu Trp Pro Pro Gln Pro

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109		180		185		190
110	Gly Gln Arg Glu Glu Cys Val Arg Lys Gly Arg Asp Pro Leu Thr Glu					
111		195		200		205
112	Cys Ala Asn Phe Val Arg Val Leu Gln Pro His Asn Arg Thr His Leu					
113		210		215		220
114	Leu Ala Cys Gly Thr Gly Ala Phe Gln Pro Thr Cys Ala Leu Ile Thr					
115	225		230		235	240
116	Val Gly His Arg Gly Glu His Val Leu His Leu Glu Pro Gly Ser Val					
117		245		250		255
118	Glu Ser Gly Arg Gly Arg Cys Pro His Glu Pro Ser Arg Pro Phe Ala					
119		260		265		270
120	Ser Thr Phe Ile Asp Gly Glu Leu Tyr Thr Gly Leu Thr Ala Asp Phe					
121		275		280		285
122	Leu Gly Arg Glu Ala Met Ile Phe Arg Ser Gly Gly Pro Arg Pro Ala					
123		290		295		300
124	Leu Arg Ser Asp Ser Asp Gln Ser Leu Leu His Asp Pro Arg Phe Val					
125	305		310		315	320
126	Met Ala Ala Arg Ile Pro Glu Asn Ser Asp Gln Asp Asn Asp Lys Val					
127		325		330		335
128	Tyr Phe Phe Phe Ser Glu Thr Val Pro Ser Pro Asp Gly Gly Ser Asn					
129		340		345		350
130	His Val Thr Val Ser Arg Val Gly Arg Val Cys Val Asn Asp Ala Gly					
131		355		360		365
132	Gly Gln Arg Val Leu Val Asn Lys Trp Ser Thr Phe Leu Lys Ala Arg					
133		370		375		380
134	Leu Val Cys Ser Val Pro Gly Pro Gly Gly Ala Glu Thr His Phe Asp					
135	385		390		395	400
136	Gln Leu Glu Asp Val Phe Leu Leu Trp Pro Lys Ala Gly Lys Ser Leu					
137		405		410		415
138	Glu Val Tyr Ala Leu Phe Ser Thr Val Ser Ala Val Phe Gln Gly Phe					
139		420		425		430
140	Ala Val Cys Val Tyr His Met Ala Asp Ile Trp Glu Val Phe Asn Gly					
141		435		440		445
142	Pro Phe Ala His Arg Asp Gly Pro Gln His Gln Trp Gly Pro Tyr Gly					
143		450		455		460
144	Gly Lys Val Pro Phe Pro Arg Pro Gly Val Cys Pro Ser Lys Met Thr					
145	465		470		475	480
146	Ala Gln Pro Gly Arg Pro Phe Gly Ser Thr Lys Asp Tyr Pro Asp Glu					
147		485		490		495
148	Val Leu Gln Phe Ala Arg Ala His Pro Leu Met Phe Trp Pro Val Arg					
149		500		505		510
150	Pro Arg His Gly Arg Pro Val Leu Val Lys Thr His Leu Ala Gln Gln					
151		515		520		525
152	Leu His Gln Ile Val Val Asp Arg Val Glu Ala Glu Asp Gly Thr Tyr					
153		530		535		540
154	Asp Val Ile Phe Leu Gly Thr Asp Ser Gly Ser Val Leu Lys Val Ile					
155	545		550		555	560
156	Ala Leu Gln Ala Gly Gly Ser Ala Glu Pro Glu Glu Val Val Leu Glu					
157		565		570		575

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158 Glu Leu Gln Val Phe Lys Val Pro Thr Pro Ile Thr Glu Met Glu Ile
 159 580 585 590
 160 Ser Val Lys Arg Gln Met Leu Tyr Val Gly Ser Arg Leu Gly Val Ala
 161 595 600 605
 162 Gln Leu Arg Leu His Gln Cys Glu Thr Tyr Gly Thr Ala Cys Ala Glu
 163 610 615 620
 164 Cys Cys Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp Gly Ala Ser Cys
 165 625 630 635 640
 166 Thr His Tyr Arg Pro Ser Leu Gly Lys Arg Arg Phe Arg Arg Gln Asp
 167 645 650 655
 168 Ile Arg His Gly Asn Pro Ala Leu Gln Cys Leu Gly Gln Ser Gln Glu
 169 660 665 670
 170 Glu Glu Ala Val Gly Leu Val Ala Ala Thr Met Val Tyr Gly Thr Glu
 171 675 680 685
 172 His Asn Ser Thr Phe Leu Glu Cys Leu Pro Lys Ser Pro Gln Ala Ala
 173 690 695 700
 174 Val Arg Trp Leu Leu Gln Arg Pro Gly Asp Glu Gly Pro Asp Gln Val
 175 705 710 715 720
 176 Lys Thr Asp Glu Arg Val Leu His Thr Glu Arg Gly Leu Leu Phe Arg
 177 725 730 735
 178 Arg Leu Ser Arg Phe Asp Ala Gly Thr Tyr Thr Cys Thr Thr Leu Glu
 179 740 745 750
 180 His Gly Phe Ser Gln Thr Val Val Arg Leu Ala Leu Val Val Ile Val
 181 755 760 765
 182 Ala Ser Gln Leu Asp Asn Leu Phe Pro Pro Glu Pro Lys Pro Glu Glu
 183 770 775 780
 184 Pro Pro Ala Arg Gly Gly Leu Ala Ser Thr Pro Pro Lys Ala Trp Tyr
 185 785 790 795 800
 186 Lys Asp Ile Leu Gln Leu Ile Gly Phe Ala Asn Leu Pro Arg Val Asp
 187 805 810 815
 188 Glu Tyr Cys Glu Arg Val Trp Cys Arg Gly Thr Thr Glu Cys Ser Gly
 189 820 825 830
 190 Cys Phe Arg Ser Arg Ser Arg Gly Lys Gln Ala Arg Gly Lys Ser Trp
 191 835 840 845
 192 Ala Gly Leu Glu Leu Gly Lys Lys Met Lys Ser Arg Val His Ala Glu
 193 850 855 860
 194 His Asn Arg Thr Pro Arg Glu Val Glu Ala Thr
 195 865 870 875

197 <210> SEQ ID NO: 3

198 <211> LENGTH: 2349

199 <212> TYPE: DNA

200 <213> ORGANISM: homo sapiens

202 <400> SEQUENCE: 3

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 205 ctgtctgcca accgctctgc catctttctg ggccccagg gctccctgaa cctccaggcc 180
 206 atgtacctag atgagtaccg agaccgcctc tttctgggtg gcctggacgc cctctactct 240
 207 ctgcggctgg accaggcatg gccagatccc cgggaggtcc tgtggccacc gcagccagga 300
 208 cagagggagg agtgtgttcg aaaggaaga gatactttga cagagtgcgc caacttcgtg 360

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Input Set : A:\LEX-0151-USA SEQLIST.txt

Output Set: N:\CRF3\09102001\I813290.raw

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209 cgggtgctac agcctcaca cgggacccac ctgctagcct gtggcactgg ggccttccag      420
210 cccacctgtg cctcatcac agttggccac cgtggggagc atgtgtccca cctggagcct      480
211 ggcagtgtgg aaagtggccg ggggcggtgc cctcacgagc ccagccgtcc ctttgccagc      540
212 accttcatag acggggagct gtacacgggt ctactgctg acttccctggg gcgagaggcc      600
213 atgatcttcc gaagtggagg tcctcgccca gctctgcgtt ccgactctga ccagagtctc      660
214 ttgcacgacc cccggtttgt gatggccgcc cggatccctg agaactctga ccaggacaat      720
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216 gtcactgtca gccgcgtggg ccgcgtctgc gtgaatgatg ctgggggcca gcgggtgctg      840
217 gtgaacaaat ggagcacttt cctcaaggcc aggtgtgtct gctcggtgcc cggccctggt      900
218 ggtgccgaga cccactttga ccagctagag gatgtgttcc tgctgtggcc caaggccggg      960
219 aagagcctcg aggtgtacgc gctgttcagc accgtcagtg ccgtgttcca gggcttcgcc      1020
220 gtctgtgtgt accacatggc agacatctgg gaggttttca acgggccctt tgcccacoga      1080
221 gatgggcctc agcaccagtg ggggccctat gggggcaagg tgcccttccc tcgcccgggc      1140
222 gtgtgccccca gcaagatgac cgcacagcca ggacggcctt ttggcagcac caaggactac      1200
223 ccagatgagg tgctgcagtt tgcccagacc caccctctca tgttctggcc tgtgcggcct      1260
224 cgacatggcc gccctgtcct tgtcaagacc cacctggccc agcagctaca ccagatcgtg      1320
225 gtggaccgcg tggaggcaga ggatgggacc tacgatgtca ttttctctgg gactgactca      1380
226 gggctctgtg tcaaagtcac cgtctccag gcagggggct cagctgaacc tgaggaagtg      1440
227 gttctggagg agctccaggt gtttaagggt ccaacacctc tcaccgaaat ggagatctct      1500
228 gtcaaaaagg aatgctata cgtgggctct cggctgggtg tggcccagct gcggctgcac      1560
229 caatgtgaga cttaacggc ctcctgtgca gagtgtctgc tggcccggga cccatactgt      1620
230 gcctgggatg gtgcctcctg taccactac cgccccagcc ttggcaagcg ccggttccgc      1680
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233 ctggagtgcc tgcccaagtc tcccargct gctgtgcgct ggctcttgca gaggccaggg      1860
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235 ctgttccgca ggcttagccg ttctgatgcg ggcacctaca cctgcaccac tctggagcat      1980
236 ggcttctccc agactgtggt ccgcctggct ctggtgtgta ttgtggcctc acagctggac      2040
237 aacctgttcc ctccggagcc aaagccagag gagccccag cccggggagg cctggcttcc      2100
238 accccaccca aggcctggtg caaggacatc ctgcagctca ttggcttcgc caacctgccc      2160
239 cgggtgggatg agtactgtga gcgcgtgtgg tgcaggggca ccacggaatg ctcaggctgc      2220
240 ttccggagcc ggagccgggg caagcaggcc aggggcaaga gctgggcagg gctggagcta      2280
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242 gccacgtag
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245 <211> LENGTH: 782
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249 <400> SEQUENCE: 4
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253 20 25 30
254 Leu Arg Leu Ser Tyr Arg Asp Leu Ser Ala Asn Arg Ser Ala Ile
255 35 40 45
256 Phe Leu Gly Pro Gln Gly Ser Leu Asn Leu Gln Ala Met Tyr Leu Asp
257 50 55 60
258 Glu Tyr Arg Asp Arg Leu Phe Leu Gly Gly Leu Asp Ala Leu Tyr Ser
259 65 70 75 80

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:16 M:270 C: Current Application Number differs, Replaced Current Application No
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:445 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:449 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7